

Figure 1

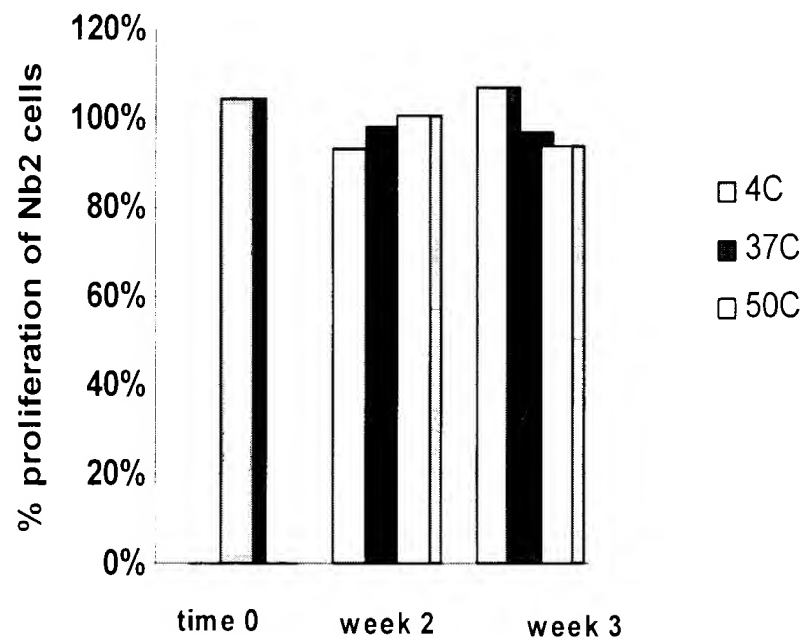


Figure 2

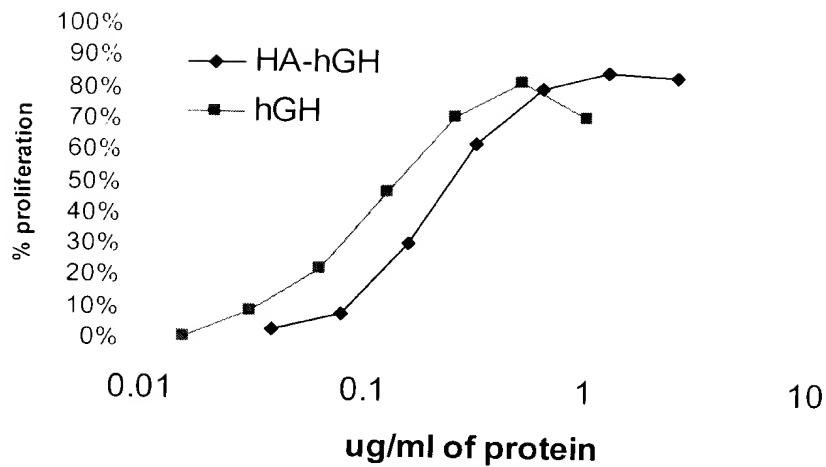


Figure 3A

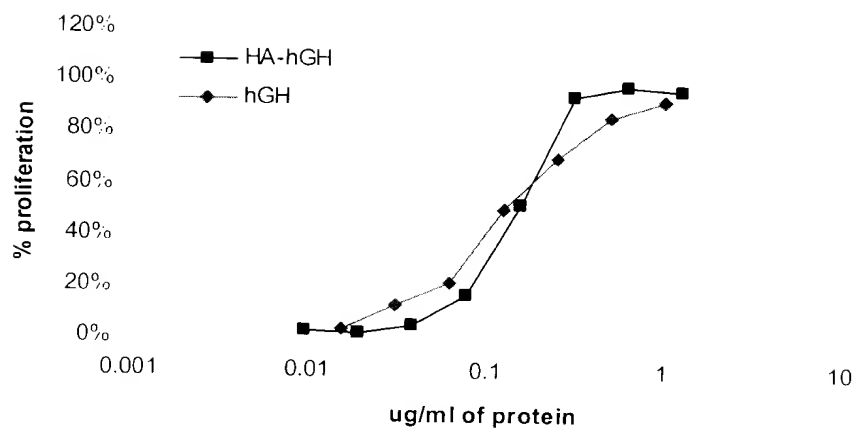


Figure 3B

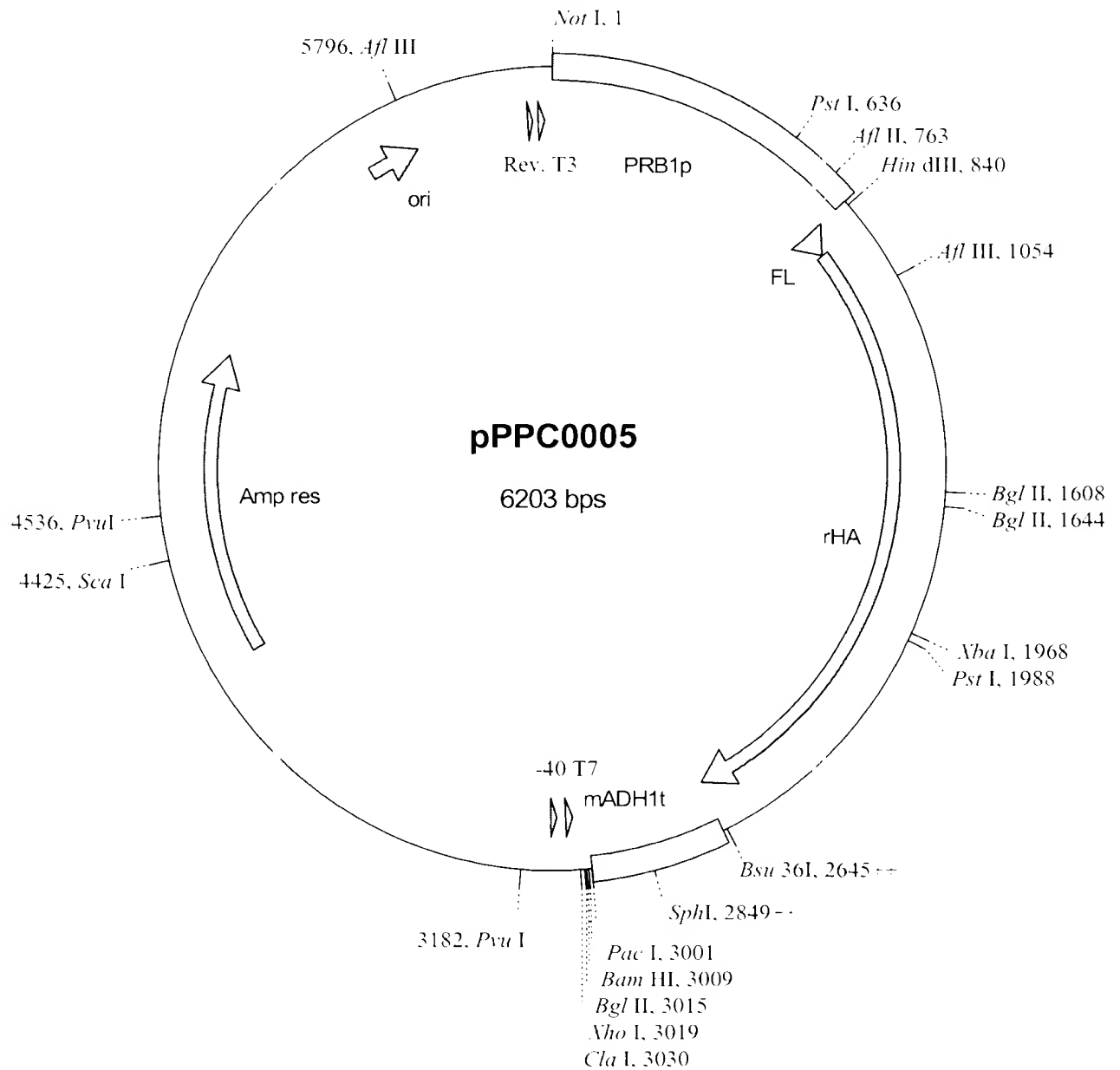


Figure 4

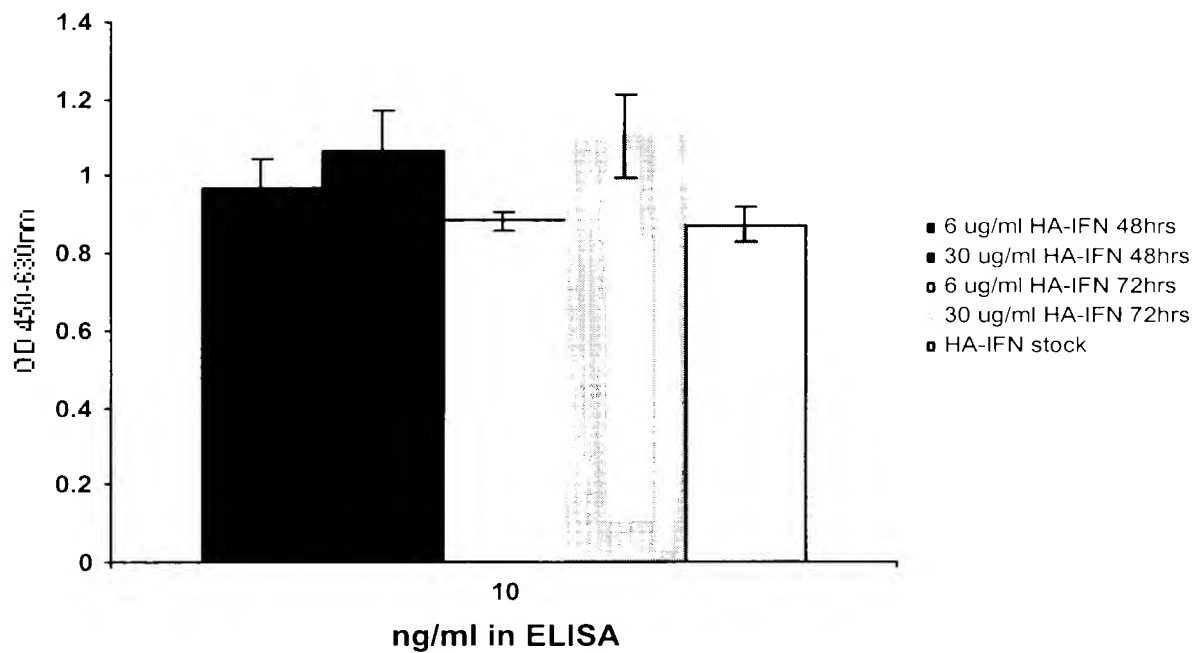


Figure 5

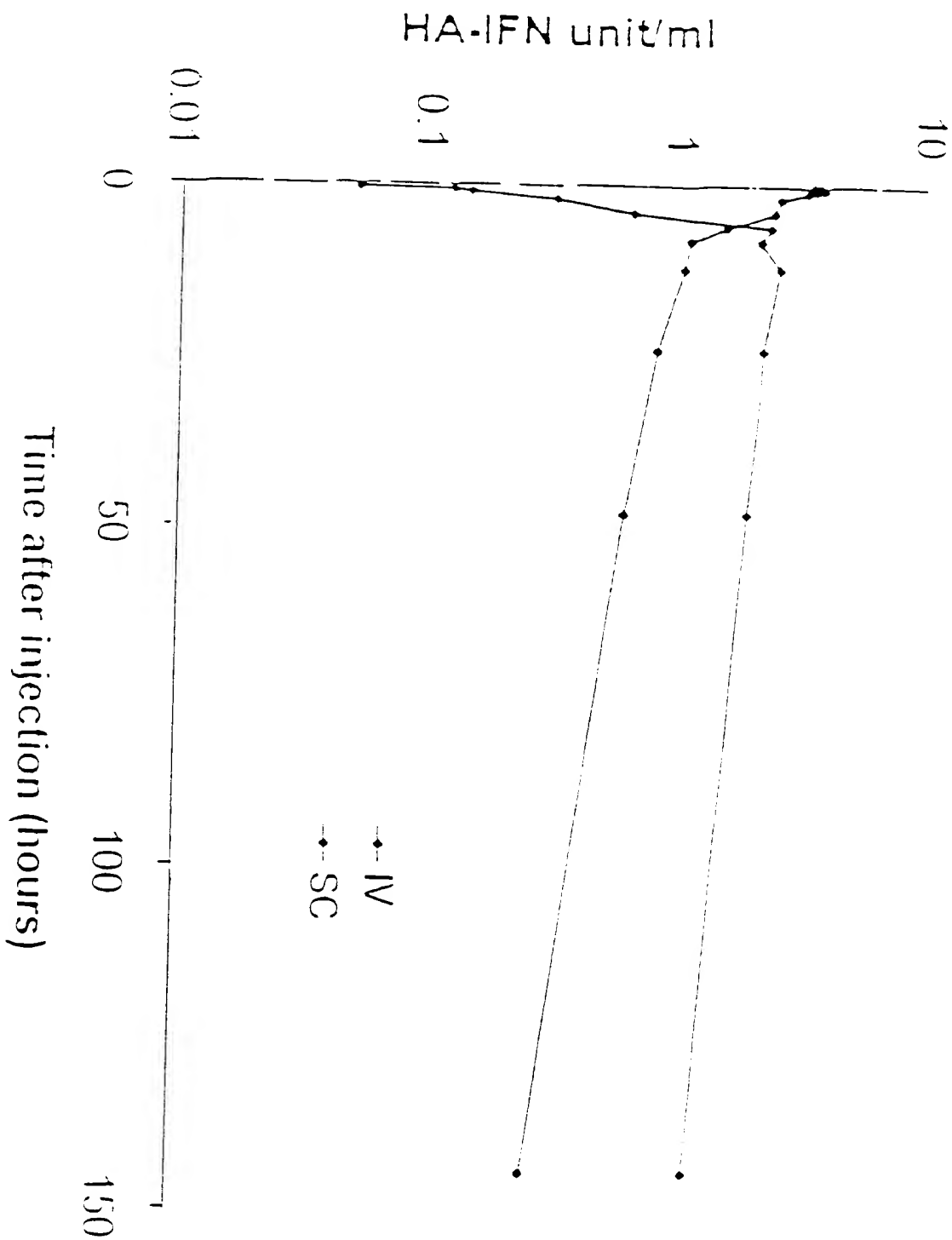


Figure 6

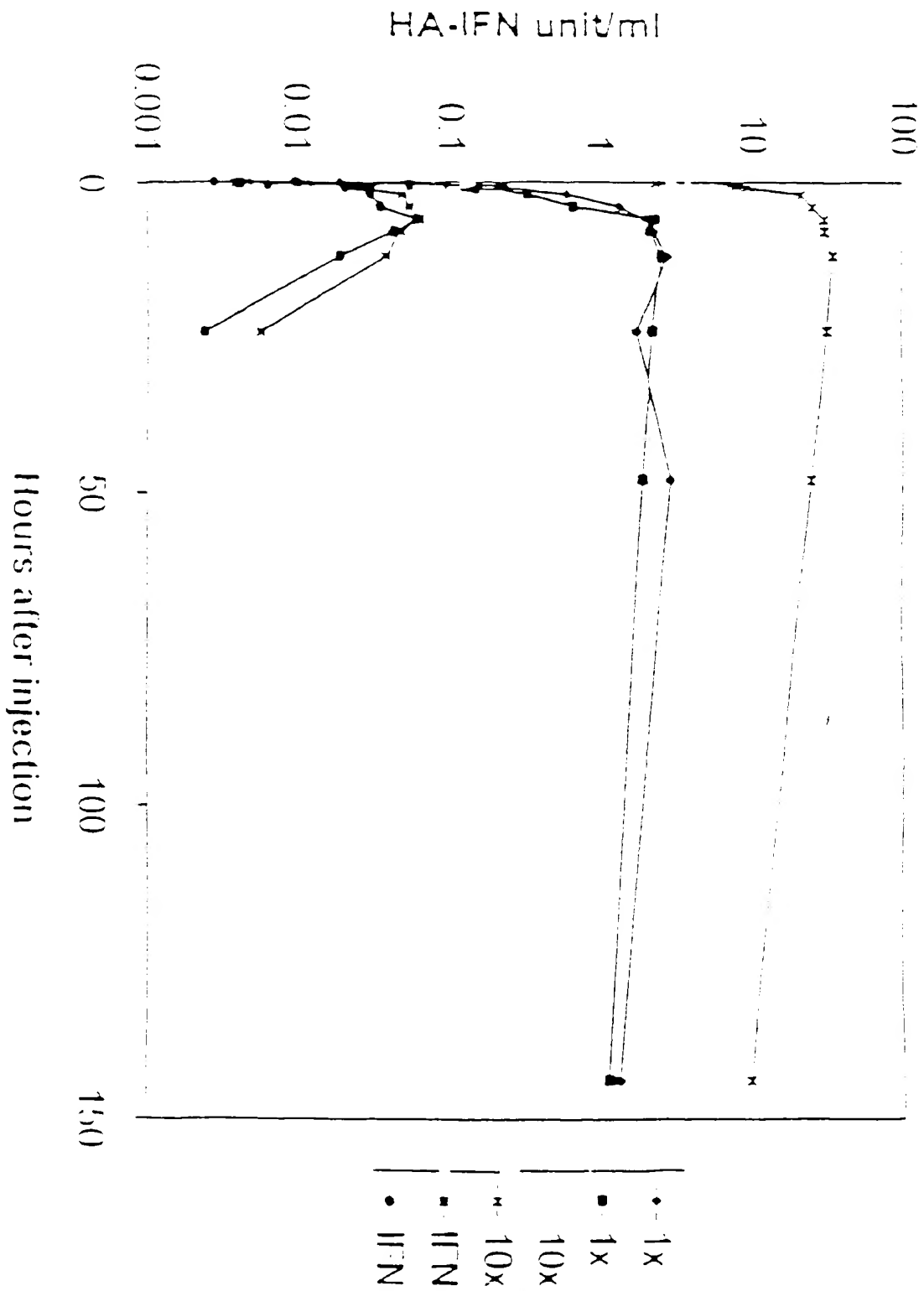


Figure 7

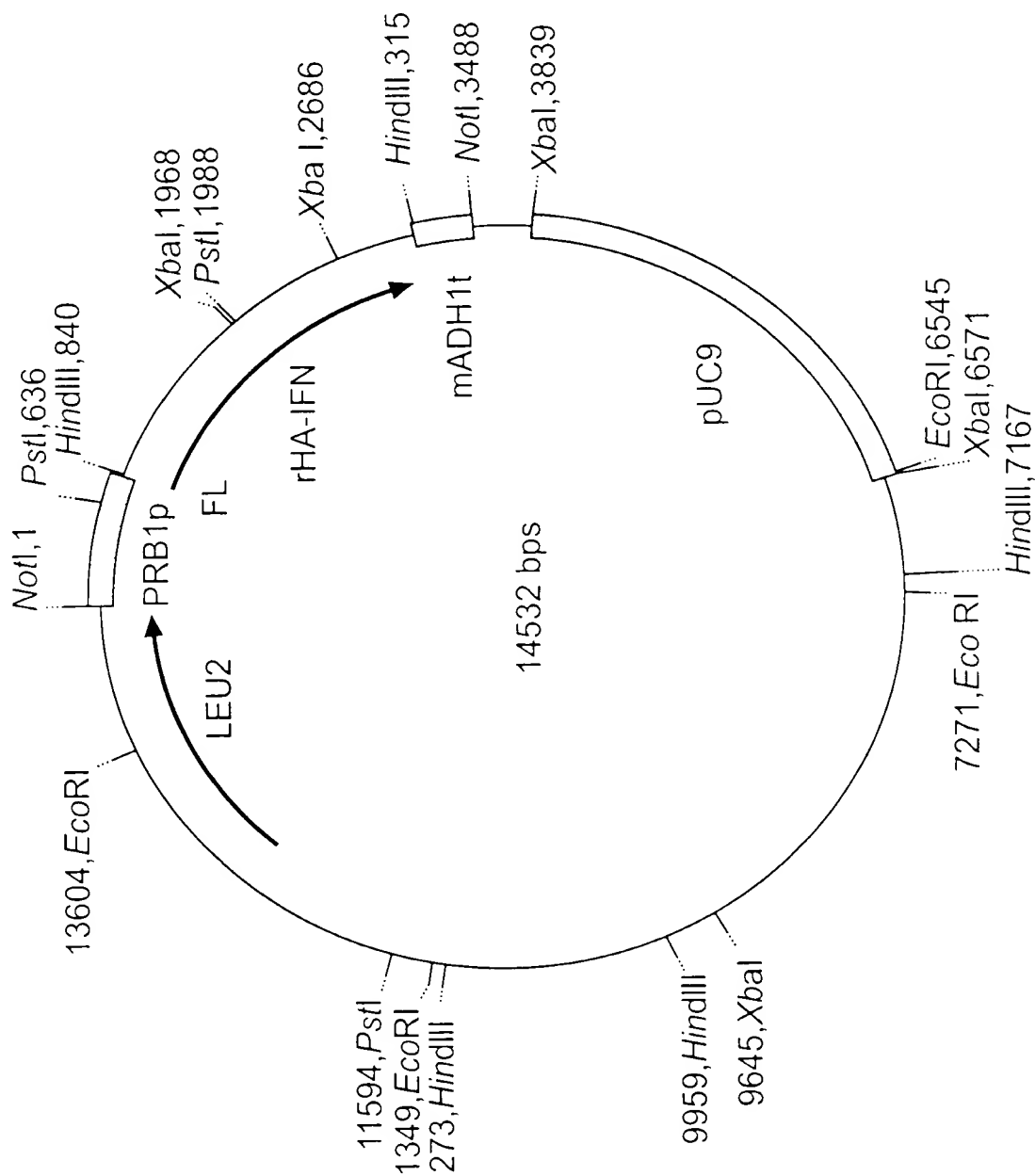


FIG. 8

Figure 9

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1    DAHKSEVAHR FKDLGEENFK ALVLIAFAQY LQQCPFEDHV KLVNEVTEFA
      HHHHH HH      HH HHHHHHHHHH      HHHHH HHHHHHHHHH

      I                      II                      III
51   KTCVADESAE NCDKSLHTLF GDKLCTVATL RETYGEMADC CAKOEPERNE
      HHHHH      HHHHH HHHHH      HHHH H      HHHH

101  CFLQHKDDNP NLPRLVRPEV DVMCTAFHDN EETFLKKYLY EIARRHPYFY
      HHHH      H      HHHHHHHH      HHHHHHHHH HHHHH

      IV
151  APELLFFAKR YKAAFTECCO AADKAACLLP KLDELRLDEGK ASSAKQRLKC
      HHHHHHHHHH HHHHHHHHH      HHHHH HHHEHHHHHH HHHHHHHHHH

      V
201  ASLQKFGERA FKAWAVARLS QRFPKAEFAE VSKLVTDLTk VHTECCHGDL
      HHHHH HH HHHHHHHHHH HH      HH HHHHHHHHHH HHHHH HH

      VI                      VII
251  LECADDRADL AKYICENODS ISSKLKECCE KPLLEKSHCI AEVENDEMPA
      HHHHHHHHHH HHHHH      HHHHH      HHHHHHH H

301  DLPSLAADFV ESKDVCKNYA EAKDVFLGMF LYEYARRHPD YSVVLLLRLLA
      HHHH      HHHHHH      HHHHHH HHHHH      HHHHHHHH

      VIII
351  KTYETTLEKC CAAADPHECY AKVFDEFKPL VEEPQNLIKQ NCELFEQLGE
      HHHHHHHHHH      HH      H      HHHHH HHHHHHHHHH HHHHHHH

      IX
401  YKFQNALLVR YTKKVPQVST PTLVEVSENL GKVGSKCCKH PEAKRMPCAE
      HHHHHHHHHH HHHH      H HHHHHHHHHH      HHH      HHHHHHHH

      X                      XI
451  DYLSVVLNQL CVLHEKTPVS DRVTKCCTES LVNRRPPCFSA LEVDETYVPK
      HHHHHHHHHH HHHHH      HHHHHHHHH      HHHHHHHH

501  EFNAETFTFH ADICTLSEKE RQIKKQTALV ELVKHKPKAT KEQLKAVMDD
      HHH      HH HHHHMEHHH HH      HHHHHHHH

      XII
551  FAAFVEKCCK ADDKETCFAE EGKKLVAASQ AALGL
      HHHHHHHH      HHHH HHHHHHHHHH HH
  
```

Loop

I Val54-Asn61
II Thr76-Asp89
III Ala92-Glu100
IV Gln170-Ala176
V His247-Glu252
VI Glu266-Glu277

Loop

VII Glu280-His288
VIII Ala362-Glu368
IX Lys439-Pro447
X Val462-Lys475
XI Thr478-Pro486
XII Lys560-Thr566

Figure 10

a. Randomisation of Loop IV.

IV
151 APELLFFAKR YKAAFTECCQ AADKAACLLP KLDEL RDEGK ASSAKQRLKC
HHHHHHHHHH HHHHHHHHH HHHHH HHHHHHHHHHH HHHHHHHHHHH

IV
151 APELLFFAKR YKAAFTECCX XXXXXXCLLP KLDEL RDEGK ASSAKQRLKC
HHHHHHHHHH HHHHHHHHH HHHHH HHHHHHHHHHH HHHHHHHHHHH

X represents the mutation of the natural amino acid to any other amino acid. One, more or all of the amino acids can be changed in this manner. This figure indicates all the residues have been changed.

b. Insertion (or replacement) of Randomised sequence into Loop IV.

(X)_n
↓
IV
151 APELLFFAKR YKAAFTECCQ AADKAACLLP KLDEL RDEGK ASSAKQRLKC
HHHHHHHHHH HHHHHHHHH HHHHH HHHHHHHHHHH HHHHHHHHHHH

The insertion can be at any point on the loop and a length where n would typically be 6, 8, 12, 20 or 25.

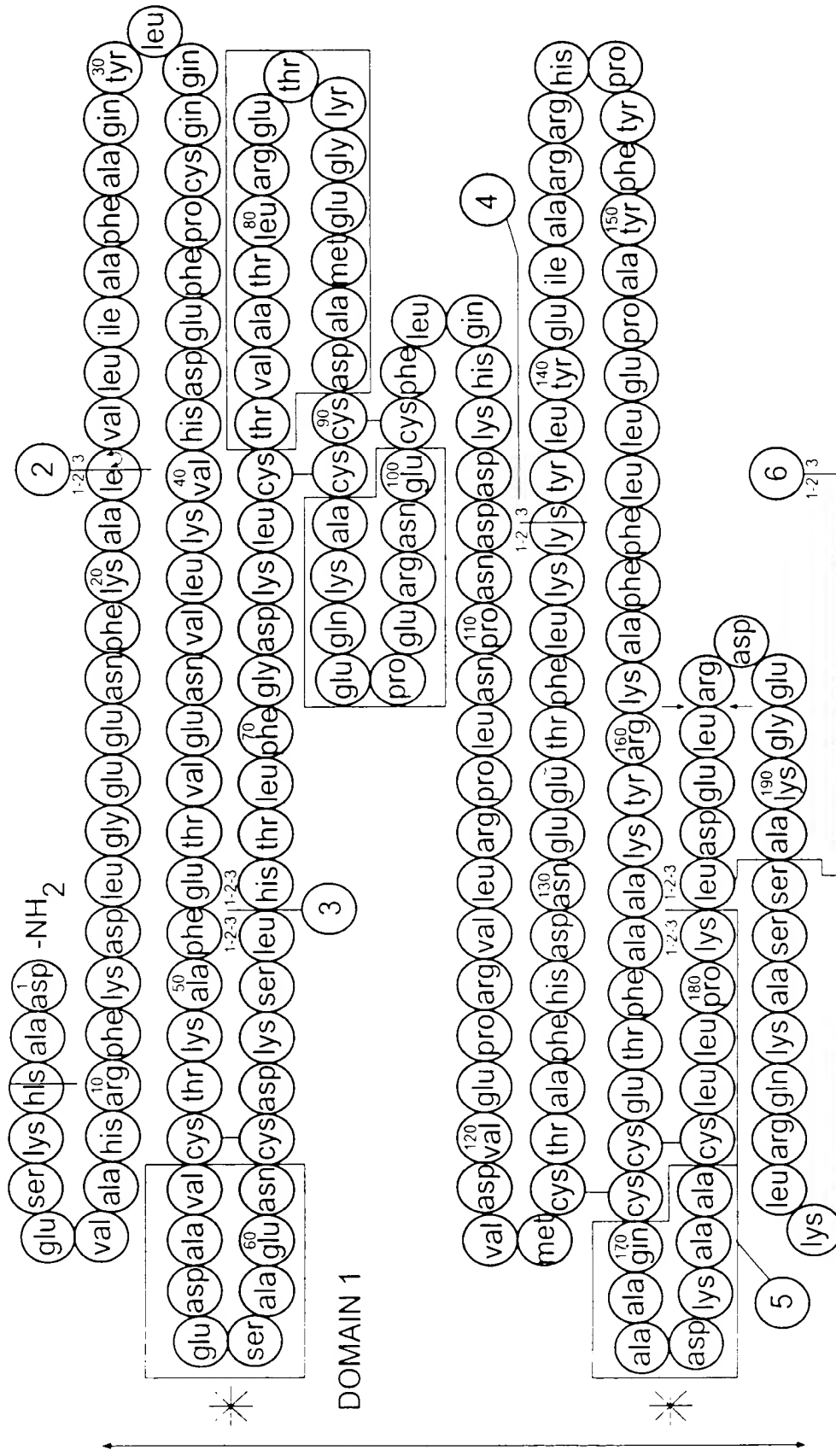


FIG. 11A

FIG. 11B

FROM FIG. 11B

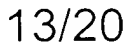


FIG. 11C



FIG. 12:
LOOP IV GLU170-A176

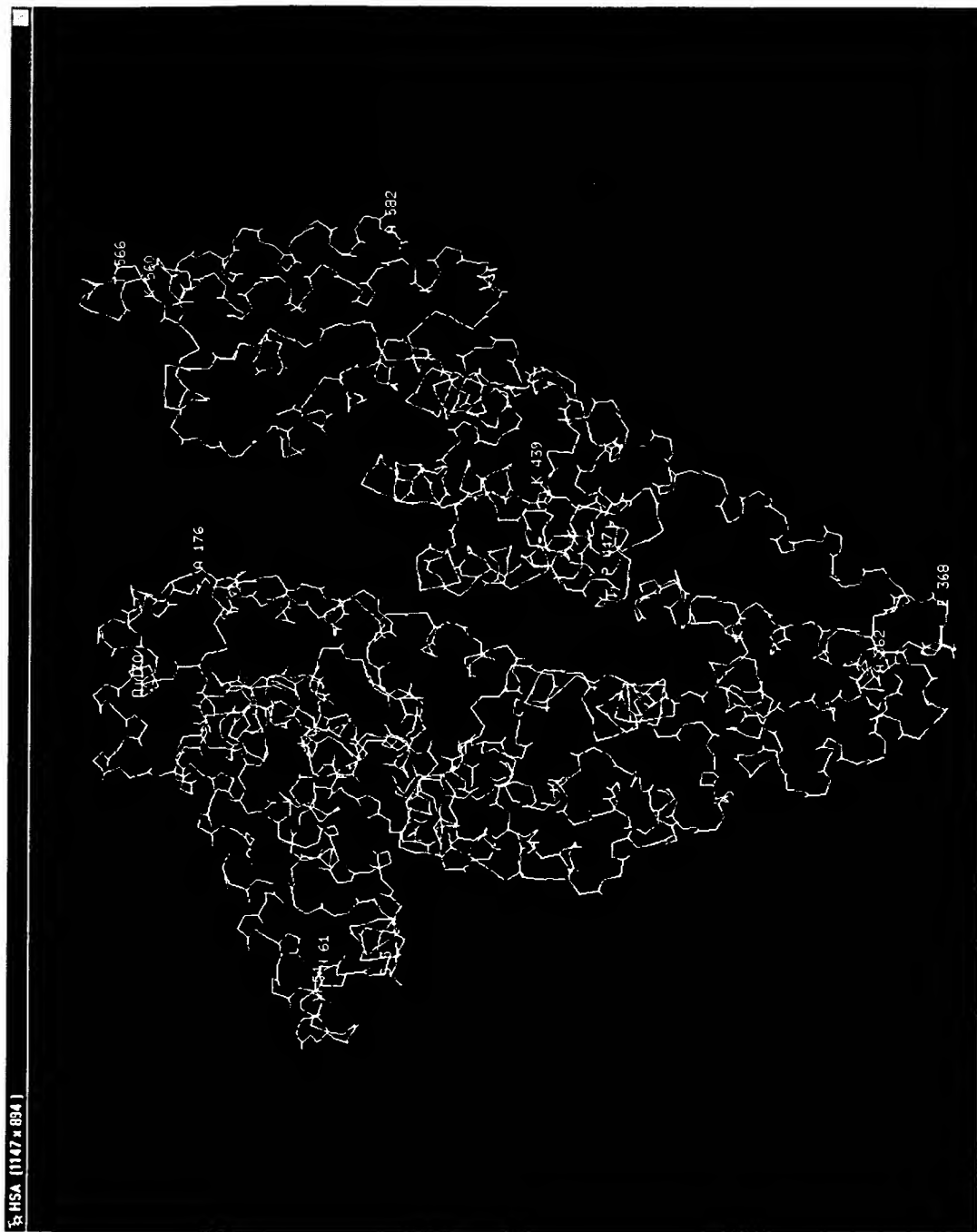


FIG. 13
TERTIARY STRUCTURE OF HSA

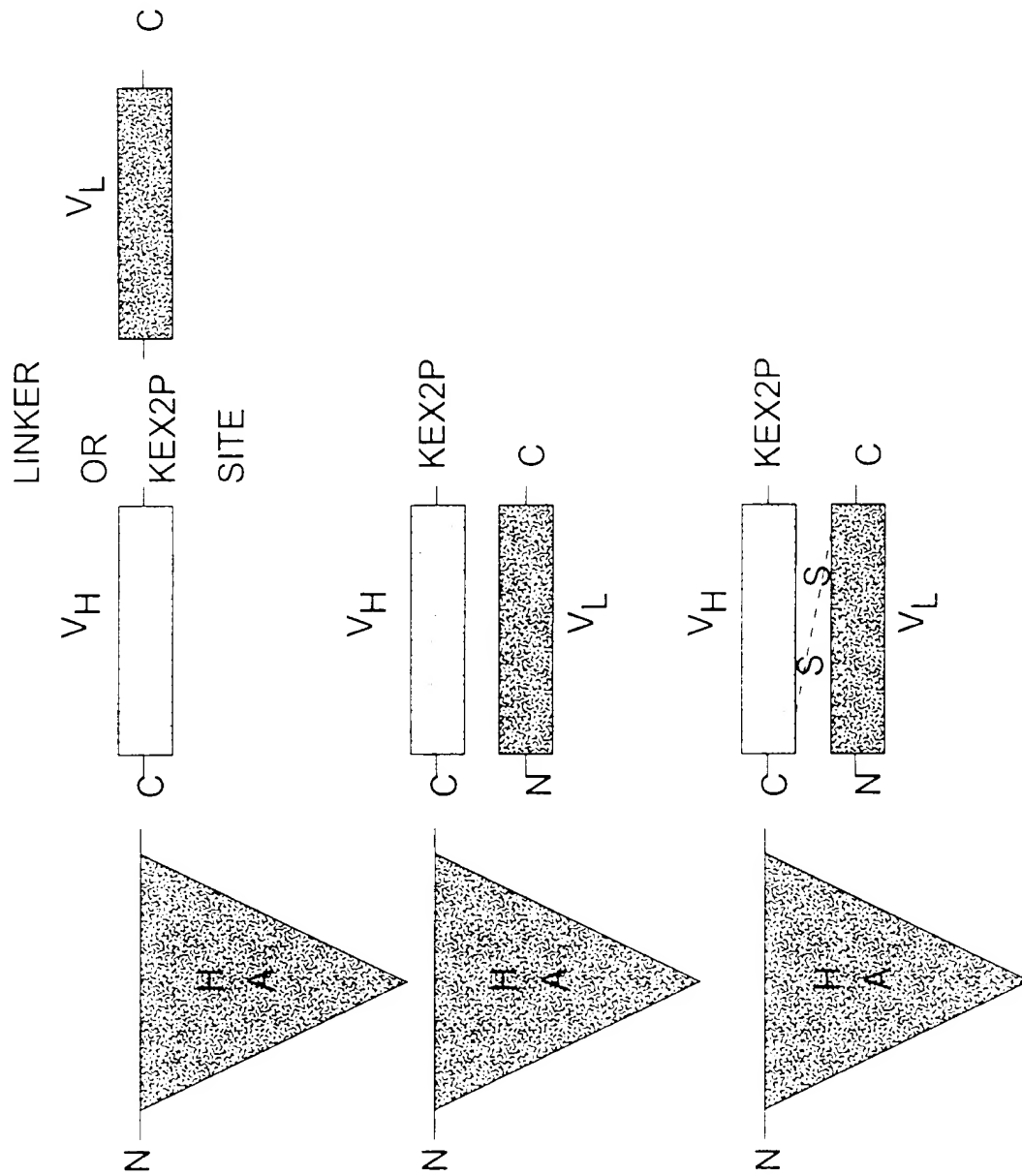


FIG. 14


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1 GAT GCA CAC AAG AGT GAG GTT GCT CAT CGG TTT AAA GAT TTG GCA GAA AAT TTC AAA 60
1 D A H K S E V A H R F K D L G E E N F K 20

61 GGC TTG GTG TTG ATT GGC TTT GCT CAG TAT CTT CAG CAG TGT CCA TTT GAA GAT CAT GTA 120
61 A L V L I A F A Q Y L Q Q C P F E D H V 40

121 AAA TTA GTG AAT GAA GTA ACT GAA TTT GCA AAA ACA TGT GGT GCT GAT GAG TCA GGT GAA 180
121 E L V H E V T E F A K T C V A D E S A E 60

181 AAT TGT GAG AAA TCA CTT CAT ACC CTT TTT GGA GAC AAA TTA TGC ACA GTT GCA ACT CTT 240
181 N C D K G L G L H T L F G D K L C T V A T L 80

241 CGT GAA ACC TAT GTT GAA ATG GCT GAC TGC TGT GCA AAA GAA CTT GAG ACA AAT GAA 300
241 P E T Y G E H A D C C A K Q E P E R N E 100

301 TGC TTC TTG CAA CAC AAA GAT GAC AAC GCA AAC CTC CCG CGA TTG GTG AGA CCA GAG GTT 360
301 C F L Q H K D D H P H L P R L V R P E V 120

361 GAT GTG ATG TGC ACT GCT TTT CAT GAC AAT GAA GAG ACA TTT TTG AAA AAA TAC TTA TAT 420
361 D V H C T A F H D H E E T F L K K Y L Y 140

421 GAA ATT GGC AGA AGA CAT CCG GAA CTC CTT TTC TTT GCT AAA AGG 480
421 E I A R R H P Y F Y A P E L L F F A K P 160

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Figure 15A

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481 TAT AAA GCT GCT TTT ACA GAA TGT TGC CAA GCT GCT GAT AAA GCT GCC TGC CTG TTG CCA 540
161 Y K A A F T E C C Q A A A D K A A C L L P 180

541 AAG CTC GAT GAA CTT CGG GAT GAA GGG AAG GCT TCG TCT GCC AAA CAG AGA CTC AAA TGT 600
181 K L D E L R D E G K A S S A K Q R L K C 200

601 GCC AGT CTC CAA AAA TTT GGA GAA AGA GCT TTC AAA GCA TGG GCA GTG GCT CGC CTG AGC 660
201 A S L Q K F G E R A F K A W A V A R L S 220

661 CAG AGA TTT CCC AAA GCT GAG TTT GCA GAA GTT TCC AAG TTA GTG ACA GAT CTT ACC AAA 720
221 Q R F P K A E F A E V S K L V T D L T K 240

721 GTC CAC ACG GAA TGC TGC CAT GGA GAT CTG CTT GAA TGT GCT GAT GAC AGG GCG GAC CTT 780
241 V H T E C C H G D L L E C A D D R A D L 260

781 GCC AAG TAT ATC TGT GAA AAT CAG GAT TCG ATC TCC AGT AAA CTG AAG GAA TGC TGT GAA 840
261 A K Y I C E N Q D S I S S K L K E C C E 280

841 AAA CCT CTG TTG GAA AAA TCC CAC TGC ATT GCC GAA GTG GAA AAT GAT GAG ATG CCT GCT 900
281 K P L L E K S H C I A E V E N D E M P A 300

901 GAC TTG CCT TCA TTA GCT GCT GAT TTT GTT GAA AGT AAG GAT GTT TGC AAA AAC TAT GCT 960
301 D L P S L A A D F V E S K D V C K N Y A 320

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Figure 15B

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961 GAG GCA AAG GAT GTC TTC CTG GGC ATG TTT TTG TAT GAA TAT GCA AGA AGG CAT CCT GAT 1020
321 E A K D V F L G M F L Y E Y A R R H P D 340

1021 TAC TGT GTC GTG CTG CTG AGA CTT GCC AAG ACA TAT GAA ACC ACT CTA GAG AAG TGC 1080
341 Y S V V L L L R L A K T Y E T T L E K C 360

1081 TGT GGC GGT GCA GAT CCT CAT GAA TGC TAT GCC AAA GTG TTC GAT GAA TTT AAA CCT CTT 1140
361 C A A A D P H E C Y A K V F D E F K P L 380

1141 GTG GAA GAG CCT CAG AAT TTA ATC AAA CAA AAC TGT GAG CAG CTT GGA GAG 1200
381 V E E P Q H L I K Q H C E L F E Q L G E 400

1201 TAC AAA TTC CAG AAT CCG CTA TTA GTT CGT TAC ACC AAG AAA GTA CCC CAA GTG TCA ACT 1260
401 Y K F Q H A L L L V P Y T K K V P Q V S T 420

1261 CCA ACT CTT GTA GAG GTC TCA AGA AAC CTA GGA AAA GTG GGC AGC AAA TGT TGT AAA CAT 1320
421 F T L V E V S R N L G K V G S K C C K H 440

1321 CCT GAA GCA AAA AAG ATG CCC TGT GCA GAA GAC TAT CTA TCC GTG GTC CTG AAC CAG TTA 1380
441 P E A K R M P C A E D Y L S V V L N Q L 460

1381 TGT GTG TTG CAT GAG AAA ACG CCA GTA AGT GAC AGA GTC ACA AAA TGC TGC ACA GAG TCC 1440
461 C V L H E K T P V S D R V T K C C T E S 480

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Figure 15C

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1441 TTG GTG AAC AGG CGA CCA TGC TTT TCA GCT CTG GAA GTC GAT GAA ACA TAC GTT CCC AAA 1500
481 L V N R R R P C F S A L E V D E T Y V P K 500

1501 GAG TTT AAT GCT GAA ACA TTC ACC TTC CAT GCA GAT ATA TGC ACA CTT TCT GAG AAG GAG 1560
501 E F N A E T F T F H A D I C T L S E K E 520

1561 AGA CAA ATC ANG AAA CAA ACT GCA CTT GTT GAG CTT GTG AAA CAC AAG CCC AAG GCA ACA 1620
521 R Q I K K Q T A L V E L V K H K P K A T 540

1621 AAA GAG CAA CTG AAA GCT GTT ATG GAT GAT TTC GCA GCT TTT GTA GAG AAG TGC TGC AAG 1680
541 K E Q L K A V M D D F A A F V E K C C K 560

1681 GCT GAC GAT AAG GAG ACC TGC TTT GCC GAG GAG GGT AAA AAA CTT GTT GCT GCA AGT CAA 1740
561 A D D K E T C F A E E G K K L V A A S Q 580

1741 GCT GCC TTA GGC TTA TAA CAT CTA CAT TTA AAA GCA TCT CAG 1782
581 A A L G L 185

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Figure 15D